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               E BEAVIS R/AU
L1          100 S E3-9
               E CHAIT B/AU
L2          244 S E3-8
L3           30 S L1 AND L2
L4           92 S L1,L2 AND LASER
L5           50 S L3-4 NOT PY>1995
L6           11 S L3-4 AND PATENT /DT
L7            3 S L1-2 AND (DISK OR ROTAT?)
L8           63 S L5-7

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L8 ANSWER 16 OF 63 CA COPYRIGHT 2003 ACS on STN
AN 121:202706 CA
TI Protein Epitope Mapping By Mass Spectrometry
AU Zhao, Yingming; **Chait, Brian T.**
CS Rockefeller University, New York, NY, 10021, USA
SO Analytical Chemistry (1994), 66(21), 3723-6
AB A mass spectrometric method is described for the rapid mapping of linear epitopes in proteins that are bound by monoclonal antibodies. The method consists of three steps. In the first step, an antigen protein is digested by a proteolytic enzyme to produce an appropriate set of peptide fragments. In the second step, peptide fragments contg. the linear epitope are selected and sepd. from the pool of peptide fragments by immunopptn. with the monoclonal antibody. In the final step, the immunopptd. peptides are identified by matrix-assisted **laser** desorption mass spectrometry. The method allows the rapid detn. of antigenic sites without tedious peptide synthesis or protein mutagenesis. The approach is demonstrated through the mapping of epitopes in 2 peptides (melittin and glucagon-like peptide-1 7-37) against which monoclonal antibodies were raised. In addn. to epitope mapping, the successful coupling between matrix-assisted **laser** desorption mass spectrometry and immunopptn. provides a potentially powerful tool for detg. binding sites between proteins.

L8 ANSWER 18 OF 63 CA COPYRIGHT 2003 ACS on STN
AN 121:103357 CA
TI Matrix-assisted **laser** desorption mass spectrometric peptide mapping of proteins separated by two-dimensional gel electrophoresis: determination of phosphorylation in synapsin I
AU Zhang, Wenzhu; Czernik, Andrew J.; Yungwirth, Tom; Aebersold, Ruedi; **Chait, Brian T.**
CS Lab. Mass Spectrom. Gaseous Ion Chem., Rockefeller Univ., New York, NY, 10021, USA
SO Protein Science (1994), 3(4), 677-86
AB A technique is described for the rapid, sensitive anal. of posttranslational modifications of proteins that have been sepd. by 2-dimensional electrophoresis and blotted onto a membrane with a cationic surface. The isolated protein spots visualized by reverse staining of the blotting membrane are excised, washed, and subjected to chem. (cyanogen bromide) and/or enzymic (endoproteinase Lys-C) degrdn. directly on the membrane. The resulting mixt. of peptide fragments is extd. from the membrane into a soln. that is compatible with matrix-assisted **laser** desorption mass spectrometric anal. and analyzed without fractionation.

Relatively accurate (±1 Da) mass detn. of these peptide fragments provides a facile and sensitive means of detecting isoforms of a given protein during 2-dimensional electrophoresis. The technique is applied to the detn. of sites of phosphorylation in synapsins Ia and Ib, neuronal phosphoproteins that are believed to function in the regulation of neurotransmitter release and are substrates for cAMP and Ca2+/calmodulin-dependent protein kinases, which appear to control their biol. activity.

L8 ANSWER 20 OF 63 CA COPYRIGHT 2003 ACS on STN
AN 120:271061 CA
TI Matrix-assisted **laser**-desorption mass spectrometry of homopolymer oligodeoxyribonucleotides. Influence of base composition on the mass spectrometric response
AU Schneider, Klaus; **Chait, Brian T.**
CS Rockefeller Univ., New York, NY, 10021, USA
SO Organic Mass Spectrometry (1993), 28(11), 1353-61
AB Matrix-assisted **laser** desorption/ionization mass spectrometry (MALDI-MS) has the potential for providing a rapid alternative to gel electrophoresis for DNA sequence anal. provided that an intense mass spectrometric response can be obtained from mixts. of DNA fragments contg. up to 300 nucleotides. MALDI-MS has not yet proved viable for such analyses because the MS response falls off rapidly for mixed-base DNA fragments contg. more than 20-30 mols. Previous studies have demonstrated that base compn. is a crit. factor in the MALDI-MS response of oligodeoxyribonucleotides. This paper describes an investigation of the phys. roots of the obsd. influence of base compn. on the mass spectrometric response, focusing on homopolymer oligodeoxyribonucleotides (dT7, dT10, dT18, dT36, dG7, dG10, dG18, dI18 and dU18) and dT5G5. Forty-eight different matrix compds. were tested for their ability to produce **laser** desorption masses spectra for such homopolymer oligodeoxyribonucleotides. Considerably stronger mass spectrometric responses were obtained for polydeoxythymidines than from polydeoxyguanosines, polydeoxycytidines and polydeoxyadenosines. Although mass spectral peaks corresponding to dT18 were obsd. from 20 of the matrixes studied, no discernible response was obsd. for dG18 from any of these matrixes. To elucidate the phys. basis for origins of the obsd. differences in response, a no. of factors were investigated including the ionization efficiency, the tendency towards fragmentation and the extent ot which the oligodeoxyribonucleotides were incorporated into the matrix crystals.

L8 ANSWER 25 OF 63 CA COPYRIGHT 2003 ACS on STN
AN 119:220922 CA
TI Protein ladder sequencing
AU **Chait, Brian T.**; Wang, Rong; **Beavis, Ronald C.**; Kent, Stephen B. H.
CS Rockefeller Univ., New York, NY, 10021, USA
SO Science (Washington, DC, United States) (1993), 262(5130), 89-92
AB A new approach to protein sequencing is described. It consists of two steps: (i) ladder-generating chem., the controlled generation from a polypeptide chain by wet chem. of a family of sequence-defining peptide fragments, each differing from the next by one amino acid; and (ii) data readout, a one-step readout of the resulting protein sequencing ladder by matrix-assisted **laser**-desorption mass spectrometry (LDMS). Each amino acid was identified from the mass difference between successive peaks, and the position in the data set defined the sequence of the original peptide chain. This method was used to directly locate a phosphoserine residue in a phosphopeptide. The protein ladder sequencing method lends itself to very high sample throughput at very low per cycle cost.

L8 ANSWER 28 OF 63 CA COPYRIGHT 2003 ACS on STN

AN 119:134753 CA
TI Analysis of synthetic proteins by matrix-assisted **laser** desorption mass spectrometry
AU **Beavis, Ronald C.**; **Chait, Brian T.**; Creel, Howard S.; Fournier, Maurille J.; Mason, Thomas L.; Tirrell, David A.
CS Lab. Mass Spectrom. Gas Phase Ion Chem., Rockefeller Univ., New York, NY, 10021, USA
SO Polymeric Materials Science and Engineering (1992), 66, 27
AB The authors report the use of matrix-assisted **laser** desorption mass spectrometry (MALDMS) in the anal. of a synthetic protein produced as part of an ongoing investigation of the crystn. behavior of periodic polypeptides. This anal. demonstrates the power of the technique for the fast, accurate detn. of mol. wt. and points the way to the use of MALDMS as a method for the sequencing of proteins.

L8 ANSWER 30 OF 63 CA COPYRIGHT 2003 ACS on STN
AN 119:2779 CA
TI Heterodimeric structure of the spider toxin ω-agatoxin IA revealed by precursor analysis and mass spectrometry
AU Santos, Ameurfina D.; Imperial, Julita S.; Chaudhary, Tanuja; **Beavis, Ronald C.**; **Chait, Brian T.**; Hunsperger, John P.; Olivera, Baldomero M.; Adams, Michael E.; Hillyard, David R.
CS Dep. Biol., Univ. Utah, Salt Lake City, UT, 84112, USA
SO Journal of Biological Chemistry (1992), 267(29), 20701-5
AB The authors report the first mol. characterization of a precursor sequence for a small, Ca2+ channel blocking, peptide spider toxin, ω-agatoxin IA. By integrating information generated from a mol. genetic approach using agatoxin cDNAs with data provided from mass spectrometry of the mature toxin, they were able to deduce the likely mechanisms by which the toxin precursor peptide is processed to its mature heterodimeric form. A particularly interesting feature of the prepropeptide is the occurrence of two glutamate-rich sequences interposed between the signal sequences, the major peptide toxin, and the minor toxin peptide. Excision of the more distal glutamate-rich region appears to be signaled by flanking arginine residues but likely occurs only after a disulfide linkage has formed between the major and minor chains of the mature toxin. This mol. genetic approach toward characterizing this toxin will allow the authors to quickly generate a series of spider sequences from which mature toxin structures can be deduced and eventually expressed. Addnl., this approach will provide insights into the evolutionary divergence obsd. among spider peptide toxins.

L8 ANSWER 34 OF 63 CA COPYRIGHT 2003 ACS on STN
AN 117:146659 CA
TI Analysis of artificial proteins by matrix-assisted **laser** desorption mass spectrometry
AU **Beavis, Ronald C.**; **Chait, Brian T.**; Creel, Howard S.; Fournier, Maurille J.; Mason, Thomas L.; Tirrell, David A.
CS Lab. Mass Spectrom. Gas Phase Ion Chem., Rockefeller Univ., New York, NY, 10021, USA
SO Journal of the American Chemical Society (1992), 114(19), 7584-5
AB An artificial protein contg. the repeated undecapeptide sequence (AlaGly)4ProGluGly was expressed in Escherichia coli and analyzed by PAGE and matrix-assisted **laser** desorption mass spectrometry. Electrophoretic anal. revealed no contaminants in the purified product but suggested a mol. wt. more than twice that expected. Accurate detn. of the mol. wt. by mass spectrometry prompted discovery of sequence errors in the DNA code for the protein, and the mass spectrum revealed the presence of small polypeptide fragments thought to be products of proteolysis. Anal. of these fragments shows that each is related to the next by addn. or

deletion of a single amino acid residue, such that portions of the protein sequence can be read directly from the mass spectrum.

L8 ANSWER 35 OF 63 CA COPYRIGHT 2003 ACS on STN
AN 117:78735 CA
TI Matrix-assisted ultraviolet **laser** desorption: evolution and principles
AU **Beavis, Ronald C.**
CS Dep. Phys., Mem. Univ. Newfoundland, St. John's, NF, A1B 3X7, Can.
SO Organic Mass Spectrometry (1992), 27(6), 653-9
AB The title topic is reviewed with 37 refs. The subjects include: sample prepn., example spectra, nomenclature, matrixes and exptl. parameters, and the mass spectrometer.

L8 ANSWER 39 OF 63 CA COPYRIGHT 2003 ACS on STN
AN 116:146840 CA
TI Matrix-assisted **laser** desorption and ionization of biomolecules
AU **Chait, Brian T.; Beavis, Ronald C.**
CS Rockefeller Univ., New York, NY, 10021, USA
SO Lecture Notes in Physics (1991), 389(Laser Ablation: Mech. Appl.), 149-53
AB A review with 9 refs., including a description of the construction and performance of a linear time-of-flight mass spectrometer with improved performance for the measurement of proteins and other biomols.

L8 ANSWER 40 OF 63 CA COPYRIGHT 2003 ACS on STN
AN 116:123530 CA
TI Investigations of matrix isolated, (UV) **laser** induced polymer sublimation using a time-of-flight mass spectrometer
AU **Beavis, R. C.; Chait, B. T.**
CS Dep. Mass Spectrom. Gas Phase Ion Chem., Rockefeller Univ., New York, NY, 10021, USA
SO NATO ASI Series, Series B: Physics (1991), 269(Methods Mech. Prod. Ions Large Mol.), 227-34
AB This paper describes a series of observations concerning the **laser**-induced polymer sublimation process using trans-3,5-dimethoxy-4-hydroxycinnamic acid (sinapic acid) as matrix. The polymers studied are bovine pancreatic insulin and horse muscle skeletal apomyoglobin.

L8 ANSWER 41 OF 63 CA COPYRIGHT 2003 ACS on STN
AN 115:251358 CA
TI Matrix assisted UV **laser** desorption of biologically interesting molecules
AU **Chait, Brian T.; Beavis, Ronald C.**
CS Rockefeller Univ., New York, NY, 10021, USA
SO Second. Ion Mass Spectrom., SIMS 7, Proc. Int. Conf., 7th (1990), Meeting Date 1989, 289-92. Editor(s): Benninghoven, Alfred. Publisher: Wiley, Chichester, UK.
AB The authors have constructed a linear time-of-flight mass spectrometer to be used for both basic research and rapid mass detns. of high mass mols. Mass resolns. of m/Δm .simeq. 500 can be obtained for small proteins (m/z <20,000), with sensitivities better than 1 pmol and mass range in excess of 100,000 u.

L8 ANSWER 42 OF 63 CA COPYRIGHT 2003 ACS on STN
AN 115:251226 CA
TI Matrix-assisted **laser** desorption/ionization mass spectrometry of biopolymers
AU Hillenkamp, Franz; Karas, Michael; **Beavis, Ronald C.; Chait, Brian T.**
CS Inst. Med. Phys., Univ. Muenster, Muenster, D-4400, Germany
SO Analytical Chemistry (1991), 63(24), 1193A-1203A
AB A review with 43 refs. about the title method with emphasis on principles, instrumentation, and application to biopolymer, (e.g., proteins, nucleic

acids, oligosaccharides) anal. in the mol. mass range between a few thousand to a few hundred thousand mass units.

L8 ANSWER 44 OF 63 CA COPYRIGHT 2003 ACS on STN
AN 115:92942 CA
TI Velocity distributions of intact high mass polypeptide molecule ions produced by matrix assisted **laser** desorption
AU **Beavis, Ronald C.; Chait, Brian T.**
CS Rockefeller Univ., New York, NY, 10021, USA
SO Chemical Physics Letters (1991), 181(5), 479-84
AB The velocity distributions of polypeptide mol. ions (mol. mass 1000-15,600 u) produced by matrix assisted UV **laser** desorption were measured using a modified time-of-flight mass spectrometer. Polypeptide mol. ions produced by matrix assisted **laser** desorption at the ion prodn. threshold irradiance have similar velocity distributions, with an av. velocity of approx. 750 m/s. This result has important implications for the design of mass spectrometers that use the effect to generate polypeptide mol. ions and for the theor. treatment of the **laser** desorption process. A jet expansion model for the desorption of high mass polymers is proposed to explain the results.

L8 ANSWER 49 OF 63 CA COPYRIGHT 2003 ACS on STN
AN 113:207759 CA
TI Rapid, sensitive analysis of protein mixtures by mass spectrometry
AU **Beavis, Ronald C.; Chait, Brian T.**
CS Dep. Mass Spectrom. Gas Phase Ion Chem., Rockefeller Univ., New York, NY, 10021, USA
SO Proceedings of the National Academy of Sciences of the United States of America (1990), 87(17), 6873-7
AB A method was developed for detg. the mol. masses of proteins in complex mixts. by mass spectrometry. The method has the capacity to examine the components of mixts. without using any chromatog. sepn. steps and will tolerate relatively large amts. of buffers and inorg. contaminants. It allows the simultaneous detn. of protein mol. masses from 1 to 40 kDa with an accuracy of ±0.01% and above 40 kDa with reduced accuracy. The lower limit for practical detection of a protein is a concn. of ≈0.1 μM, and <1 μL of such a soln. is consumed. The anal. is very fast: <15 min is necessary to perform the complete anal., including sample prepn., introduction into the mass spectrometer, mass spectrum collection, and data redn. The mass spectrum that is obtained does not require elaborate interpretation because there is no fragmentation of the ionized protein (or protein subunit) mol. Therefore, there is a one-to-one correspondence between the peaks in the mass spectrum and the proteins present in the original mixt. The spectra assume the appearance of chromatograms, with the abscissa being mass-to-charge ratio rather than chromatog. retention time.

L8 ANSWER 50 OF 63 CA COPYRIGHT 2003 ACS on STN
AN 113:74080 CA
TI High-accuracy molecular mass determination of proteins using matrix-assisted **laser** desorption mass spectrometry
AU **Beavis, Ronald C.; Chait, Brian T.**
CS Dep. Mass Spectrom. Gas, Phase Ion Chem., Rockefeller Univ., New York, NY, 10021, USA
SO Analytical Chemistry (1990), 62(17), 1836-40
AB A method for obtaining protein mol. masses with an accuracy of approx. ±0.01% by matrix-assisted **laser** desorption using an internal calibrant is described. The technique allows accurate mass detns. of protein sample sizes as small as 1 pmol. High concns. of org. and inorg. contaminants (e.g., 1M urea) do not strongly affect either the signal

intensity or the mass assignment. The ability to assign an accurate mol. mass to a protein is contingent on the observation of clearly resolved protonated mol. ions in the mass spectrum.

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* Rapid comm. Mass Spec, 1989, 3, 233

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